RAW SEQUENCE LISTING
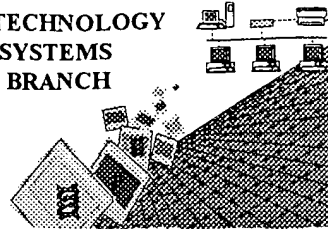# ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09//05,//7 J_

Source: _/602_

Date Processed by STIC: _/2/13/2002_

RECEIVED

JAN 0 2 2003

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

1600

RAW SEQUENCE LISTING   DATE: 12/13/2002
PATENT APPLICATION: US/09/105,117J   TIME: 15:15:03

Input Set : A:\Seq_listing_US_korrigiert141102.txt
Output Set: N:\CRF4\12132002\I105117J.raw

```
    3 <110> APPLICANT: Forschungszentrum Juelich GmbH
    5 <120> TITLE OF INVENTION: Process for the microbial production of amino acids by
    6        boosted activity of export carriers
    8 <130> FILE REFERENCE: 1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/105,117J
   11 <141> CURRENT FILING DATE: 1998-06-17
   13 <160> NUMBER OF SEQ ID NOS: 5
   15 <170> SOFTWARE: PatentIn Ver. 2.0
```

All following pages for Explanation

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
E--> 208 <210> SEQ ID NO: (complement to <210> 1)
   209 <221> NAME/KEY: unsure
   210 <222> LOCATION: CDS (2)..(652)
   211 <223> OTHER INFORMATION: orf3
W--> 212 <220> FEATURE:
   213 <221> NAME/KEY: gene
   214 <222> LOCATION: CDS (1421)..(2293)
   215 <223> OTHER INFORMATION: LysG
W--> 217 <400> 3
   218 a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg 49
   219   Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
   220    1              5                  10                 15
   222 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc   97
   223 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
   224              20                  25                 30
   226 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg  145
   227 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
   228              35              ·   40                 45
   230 att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg  193
   231 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
   232      50                  55                  60
   234 ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt  241
   235 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
   236  65                  70                  75                  80
   238 ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa  289
   239 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
   240              85                  90                  95
   242 tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc  337
   243 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
   244             100                 105                 110
   246 ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag  385
```

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> Process for the microbial production of amino acids by
      boosted activity of export carriers

<130> 1

<140> US/09/105,117 (PCT/DE96/02485)
<141> 1998-06-17
<150>
<151>
<160> 5

<170> PatentIn Ver. 2.0

<210> 1
<211> 2374
<212> DNA
<213> Corynebacterium glutamicum
<220> (LysE)
<221> gene
<222> CDS (1016)..(1726)
<223>
<400> 1

ccatttgctg aaggtgttac tctgcctggc ccaattcctg cgggcgaaga agtgaaaaac 60

cctgaacctt ttcagaagta actaaggccg caatccctcg attgctgcat caacgacggc 120

gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180

gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240

ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttccgc 300

cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360

acggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcatcgcag cccaatctag 420

tttcccatca accatgtagg catcccgcaa tgaggggggtt gcaatggcca agtggcgcat 480

ggttccaagt tctactactt cacatcccgc cacgggatta gcttcacggg ttaccgctcc 540

taaaacatct ccacgccgca gcaaggataa tgtgtgcgct tcatcttcca agcgcagcgt 600

gagcgttgct ccaccccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660

cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttgcgc 720

tttagtttct gcttgcagca acaccatttt ccgcgctgct tgcacaagga cttcacccgc 780

ttcggttgct ttggccggtt gggtgcgcga taccaacact cgacccacgt gatgctcgag 840

agctttaacg cgctgactca ccgccgaggg ggaaatggaa agggctaagg aggcgccttc 900

gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatggggt tcatgaagct 960

```
atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg    1018
                                                                 Met
                                                                  1

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt    1066
Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu
                  5                  10                  15

tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att    1114
Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile
              20                  25                  30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac    1162
Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp
     35                  40                  45

gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat    1210
Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn
 50                  55                  60                  65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac    1258
Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr
                  70                  75                  80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag    1306
Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys
              85                  90                  95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat    1354
Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
             100                 105                 110

gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg    1402
Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
         115                 120                 125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc    1450
Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
130                 135                 140                 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg    1498
Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
             150                 155                 160

gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc    1546
Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
             165                 170                 175

gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg    1594
Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
         180                 185                 190

ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc    1642
Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
         195                 200                 205
```

```
agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg   1690
Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
210                 215                 220                 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg        1736
Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
                230                 235

ttttggaatc ggtggccttc gcccaaatgt tgatgccggc gtcgtgggaa atctcatcga 1796

tcgcctccaa ctcggcgtca gaaaactcca agttgttgag tgaatcaagg ctgttgtcca 1856

gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgcg ccgtactctc 1916

cttgctcgcg cagcacccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976

cgatgtcatt gagcttgcgg accatatcaa tattgttcac gttcaacatg ccctcagaca 2036

gggacttacc ctggctggcg cgggaaccct ctggaattcc atcgagatat ttgtccgtga 2096

gcaggccctg cgcaagtggt gagaaagcaa tgacgccaag accattgttg gcagctgact 2156

gcaacaagtt ctcaccgtca tcgcccggtt cctccaccca acgattaatg atggaatagc 2216

ttggctgatg aatcagaagc gggcagccct cctccgccat gaactcagcc gcctccgctg 2276

tgagctctgg accgtaggaa gaaataccca cgtaaagagc ctttccagac gcaacaatgt 2336

cacgcaatgc gtacatggtt tcttccaaag gagtatct                          2374
```

```
<210> 2
<211> 236
<212> PRT
<213> Corynebacterium glutamicum
<220> (LysE)
<223>
<400> 2
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
  1               5                  10                  15

Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
           20                  25                  30

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
        35                  40                  45

Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
     50                  55                  60

Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
 65                  70                  75                  80

Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
                85                  90                  95
```

```
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
            100                 105                 110

Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
            115                 120                 125

Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
        130                 135                 140

Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
145                 150                 155                 160

Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
                165                 170                 175

Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
            180                 185                 190

Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
            195                 200                 205

Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
        210                 215                 220

Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
225                 230                 235
```

```
<210> 3
<211> 2374
<212> DNA
<213> Corynebacterium glutamicum
<220> (complement to <210> 1)
<221> unsure
<222> CDS (2)..(652)
<223> orf3
<220>
<221> gene
<222> CDS (1421)..(2293)
<223> LysG

<400> 3
a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg    49
  Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
   1               5                  10                  15

tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc    97
Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
            20                  25                  30

aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg   145
Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
        35                  40                  45
```

(complement to SEQ ID No 1) please use this format instead of <210> 1; otherwise, the CRF software interprets <210> 1 as a new sequence

```
att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg   193
Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
        50              55                  60

ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt   241
Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
65                      70                  75                  80

ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa   289
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
                85                  90                  95

tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc   337
Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
                100                 105                 110

ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag   385
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
        115                 120                 125

ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg   433
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
    130                 135                 140

ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg   481
Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
145                 150                 155                 160

acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc   529
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
                165                 170                 175

ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg   577
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
                180                 185                 190

atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc   625
Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
            195                 200                 205

acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat          672
Thr Asp Ser Lys Thr Arg Glu Asn
    210                 215

ggccaatgcg gtcatcacaa ctgccacgac gacgttgatc cagcgccaca ccttggggct   732

ggacagcggg cgtgacaatg ctgctgcgcc gaaacccacc agcgggaacc agatcaggct   792

tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac   852

gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat   912

tgccatcaac atgggcttta cccaaacccg ctgcttatcg acgctcacct ccacccgcac   972

ccggttgcgc gtgtcagtgg ccaccgccga accgcccaaa ggcgtgtcat cgggcacggt   1032
```

```
tggttctgtt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtctttcgc 1092

tgccatgacg gcaaaccata acaggtaagc gatgccaccc cagcgcataa tatcgagcac 1152

gatcggcgcg gcattggaca aaagatcaac gcccaaggtg ccggcgatga acaaaaagac 1212

gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttgttt 1272

aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggccccca aaagcagacc 1332

tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392

ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act      1444
                                Met Asn Pro Ile Gln Leu Asp Thr
                                         220                 225

ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc   1492
Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala
                  230                 235                 240

ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag   1540
Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu
              245                 250                 255

cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca   1588
His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala
          260                 265                 270

acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg   1636
Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu
      275                 280                 285

ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc   1684
Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile
290                 295                 300                 305

ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct   1732
Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro
                  310                 315                 320

ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg   1780
Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu
              325                 330                 335

cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat   1828
Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp
          340                 345                 350

gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa   1876
Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu
      355                 360                 365

gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca   1924
Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser
370                 375                 380                 385

ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gcg atg   1972
Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
```

```
Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
              390                 395                 400

ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg    2020
Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu
              405                 410                 415

gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc    2068
Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val
              420                 425                 430

ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg    2116
Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp
        435                 440                 445

gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa    2164
Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu
450                 455                 460                 465

gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa    2212
Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln
                  470                 475                 480

cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc    2260
Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val
              485                 490                 495

gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag  2313
Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
              500                 505

ggttttcac ttcttcgccc gcaggaattg ggccaggcag agtaacacct tcagcaaatg   2373

g                                                                  2374


<210> 4
<211> 216
<212> PRT
<213> Corynebacterium glutamicum
<220> (orf3)
<223>
<400> 4
Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
  1               5                  10                  15

Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
              20                  25                  30

Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
              35                  40                  45

Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
       50                  55                  60

Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
  65                  70                  75                  80
```

```
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
              85                  90                  95

Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
              100                 105                 110

Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
              115                 120                 125

Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
        130                 135                 140

Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
145                 150                 155                 160

Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
              165                 170                 175

Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
              180                 185                 190

Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
        195                 200                 205

Thr Asp Ser Lys Thr Arg Glu Asn
        210                 215


<210> 5
<211> 290
<212> PRT
<213> Corynebacterium glutamicum
<220> (LysG)
<223>
<400> 5
Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
  1               5                  10                  15

Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
              20                  25                  30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
          35                  40                  45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
      50                  55                  60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
65                  70                  75                  80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
              85                  90                  95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
              100                 105                 110
```

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
    115   120   125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
    130   135   140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
145   150   155   160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
             165   170   175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
        180   185   190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
        195   200   205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
    210   215   220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
225   230   235   240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
        245   250   255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
        260   265   270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
        275   280   285

Arg Pro
    290

FZJ 9910 PCT/US   8/8   12.11.02
US 09/105,117

delete